Amendments to the Claim:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-92 (cancelled).

93 (currently amended). A recombinant ~~microbial~~ yeast cell comprising:

i) at least one increased expressible yeast enzyme activity controlling anabolic metabolism of ammonia in said cell as a nutrient source, said increased enzyme activity being ~~an NADH-dependent activity catalysing a reaction~~ selected from the group consisting of:

(a) a glutamate dehydrogenase activity catalyzing the reaction:

2-oxoglutarate + NH_4^+ + NADH → glutamate + NAD^+

and being that encoded by GDH2 of Saccharomyces cerevisiae;

(b) a glutamate synthase activity catalyzing the reaction:

2-oxoglutarate + glutamine + NADH → 2 glutamate + NAD^+

and being that encoded by GLT1 of Saccharomyces cerevisiae; and

(c) a glutamine synthetase activity catalyzing the reaction:

glutamate + NH_4^+ + ATP → glutamine + ADP + Pi

and being that encoded by GLN1 of Saccharomyces cerevisiae;

wherein each increased enzyme activity is that of (1) an enzyme, endogenous to said cell, encoded by a nucleic acid coding sequence operably linked to at least one regulatory sequence not natively associated with said nucleic acid coding sequence, whose expression is increased as compared to the expression of the enzyme activity when said nucleic acid coding sequence is associated with its native regulatory sequence or (2) an enzyme,

exogenous to said cell, encoded by a nucleic acid coding sequence, operably linked to at least one regulatory sequence, and wherein the recombinant ~~bacterial~~ yeast cell is further characterized by

ii) a reduced expressible enzyme activity controlling anabolic metabolism of ammonia in said cell as a nutrient source, said reduced enzyme activity being a natively present NADPH-dependent glutamate dehydrogenase activity which ~~native~~ reduced activity is ~~that of a native enzyme encoded by a native nucleic acid coding sequence, and being~~ reduced compared to the native level of activity~~,~~ ~~wherein said microbial cell is a fungal cell~~.

94 (currently amended). The ~~microbial~~ yeast cell of claim 93, said cell comprising an increased ~~expressible~~ enzyme activity ~~catalysing reaction~~ (b) and ~~second~~ an increased ~~expressible~~ enzyme activity ~~catalysing reaction~~ (c).

95 (currently amended). The ~~microbial~~ yeast cell of claim 93, said cell comprising a further increased expressible enzyme activity, said further expressible enzyme activity being the pyridine nucleotide transhydrogenase activity encoded by CTH of Azobacter vinelandii as harboured by Saccharomyces cerevisiae TN4 deposited under DSM Accession No. 12267 ~~controlling an intracellular redox system of said cell, said further expressible enzyme activity~~ and being operably linked to a regulatory sequence not natively associated with said further enzyme activity in said yeast cell.

96-98 (cancelled).

99 (currently amended). The ~~microbial~~ yeast cell of claim ~~98~~ 95, wherein said intra-cellular transhydrogenase activity is heterologous to said cell.

100 (cancelled).

101 (currently amended). The ~~microbial~~ yeast cell of claim 99, wherein said cell comprises no endogenous transhydrogenase activity.

102 (cancelled).

103 (currently amended). The ~~microbial~~ yeast cell of claim 93, comprising an increased ~~expressible~~ enzyme activity (b) ~~catalysing reaction (b) which is provided by a glutamate synthase~~.

104 (cancelled).

105 (currently amended). The ~~microbial~~ yeast cell of claim ~~104~~ 103, wherein said ~~glutamate synthase in that encoded by~~ GLT1 is that of the strain of *Saccharomyses cerevisiae* ~~as~~ deposited under DSM Accession No. 12275.

106 (currently amended). The ~~microbial~~ yeast cell of claim 93, comprising an increased ~~expressible~~ enzyme activity ~~catalysing reaction~~ (c)~~, which is provided by a glutamine synthetase~~.

107 (cancelled).

108 (currently amended). The ~~microbial~~ yeast cell of claim ~~107~~ 106, wherein said ~~glutamine synthetase is~~ GLN1 is that of the strain of *Saccharomyces cerevisiae* ~~as~~ deposited under DSM Accession No. 12274.

109 (currently amended). The ~~microbial~~ yeast cell of claim 93, comprising an increased ~~expressible~~ enzyme activity ~~catalysing reaction~~ (a)~~, wherein said increased enzyme activity is a *Saccharomyces cerevisiae* glutamate dehydrogenase activity~~.

110 (cancelled).

111 (currently amended). The ~~microbial~~ yeast cell of claim ~~110~~ 109, wherein said GDH2 ~~glutamate dehydrogenase activity~~ is that of the strain of *Saccharomyces cerevisiae* ~~TN22~~ deposited under DSM Accession No. 12277.

112 (currently amended). The yeast cell of claim 93 in which said reduced enzyme activity is the result of deletion of at least part of the native nucleic acid coding sequence of (ii), and/or of at least part of at least one natively associated regulatory sequence.

113 (cancelled).

114 (currently amended). The ~~microbial~~ yeast cell of claim

~~113~~ 93, which is a genetically modified *Saccharomyces, Schizosaccharomyces or Pichia* yeast.

115 (currently amended). The ~~microbial~~ yeast cell of claim 93, said cell being *Saccharomyces cerevisiae* TM 19 as deposited under Accession No. DSM 12276.

116 (currently amended). The ~~microbial~~ yeast cell of claim 93, said cell being *Saccharomyces cerevisiae* TN22 as deposited under Accession No. DSM 12277.

117 (currently amended). The ~~microbial~~ yeast cell of claim 93, in the form of a frozen or freeze-dried preparation.

118 (currently amended). The ~~microbial~~ yeast cell of claim 117, said cell being partly or wholly reconstitutable.

119 (currently amended). A composition comprising the ~~microbial~~ yeast cell according to claim 93, in a carrier.

120 (previously presented). The composition of claim 119, wherein the carrier is a physiologically acceptable carrier.

121 (previously presented). The composition of claim 119, said composition being a fermentation starter culture.

122 (currently amended). The ~~microbial~~ yeast cell of claim 93, wherein production of a first metabolite is substantially increased as compared to a ~~microbial~~ yeast cell which is identical to the claimed cell except that it lacks ~~at least one of~~ (i) ~~or~~ and (ii).

123 (currently amended). The ~~microbial~~ yeast cell of claim 122, wherein said production of said first metabolite is increased by a factor of at least 1.08.

124 (currently amended). The ~~microbial~~ yeast cell of claim 122, wherein said first metabolite is ethanol.

125 (currently amended). The ~~microbial~~ yeast cell of claim 122, further producing a second metabolite, the production of said metabolite being substantially decreased as compared to the production of said second metabolite in a comparable wild-type cell or a comparable isolated ~~microbial~~ yeast cell, said comparable wild type cell or comparable isolated ~~microbial~~ yeast cell being identical to the claimed cell except that said

comparable wild type cell or comparable isolated ~~microbial~~ yeast cell lacks said increased expressible enzyme activity (i) and does not have said further characterising reduction of natively present NADPH-dependent hydrogenase activity.

126 (currently amended). The ~~microbial~~ yeast cell of claim 125, wherein said second metabolite is glycerol.

127 (currently amended). A method of producing a first metabolite, said method comprising the steps of i) cultivating a ~~microbial~~ yeast cell according to claim 122 in a suitable growth medium and under such conditions that said ~~microbial~~ yeast cell produces said first metabolite and optionally ii) isolating said first metabolite in a suitable form, and further optionally iii) purifying said isolated first metabolite.

128 (currently amended). A method of constructing a ~~microbial~~ yeast cell according to claim 122, said method comprising the steps of i) operably linking a nucleotide sequence encoding an enzyme mediating said increased expressible enzyme activity with an expression signal not natively associated with said nucleotide sequence, and reducing or eliminating said reduced or eliminated expressible enzyme activity from said ~~microbial~~ yeast cell.

129 (previously presented). The method of claim 128, wherein said reduced or eliminated enzyme activity is reduced or eliminated by operably linking a nucleotide sequence encoding an enzyme mediating for said expressible enzyme activity with a regulatory sequence not natively associated with said nucleotide sequence, said regulatory sequence generating a reduced expression of said nucleotide sequence.

130 (currently amended). The yeast cell of claim 93 in which at least one such regulatory sequence not natively associated with said coding sequence is a promoter.

131 (currently amended). The yeast cell of claim 93 in which the reduced enzyme activity is an eliminated activity.

132 (currently amended). The yeast cell of claim 93 in which at least one ~~such~~ said increased enzyme activity is that

of an enzyme endogenous to the cell.

133 (currently amended). The yeast cell of claim 132 in which said endogenous enzyme is encoded by its native coding sequence.

134 (currently amended). The yeast cell of claim 93 in which said reduced enzyme activity is the result of operably linking least one regulatory sequence, not natively associated with the coding sequence encoding the native enzyme of (ii), with said native nucleic acid coding sequence, so that expression of said native enzyme is reduced.

135 (currently amended). The yeast cell of claim 93 in which said reduced enzyme activity is the result of repression of expression.

136 (new). The recombinant yeast cell of claim 93, comprising:

i) at least one increased expressible yeast enzyme activity controlling anabolic metabolism of ammonia in said cell as a nutrient source, said increased enzyme activity being selected from the group consisting of:

(a) a glutamate dehydrogenase activity catalyzing the reaction:

2-oxoglutarate + NH_4^+ + NADH → glutamate + NAD^+

and being that encoded by GDH2 of the strain of *Saccharomyces cerevisiae* deposited under DSM Accession No. 12277;

(b) a glutamate synthase activity catalyzing the reaction:

2-oxoglutarate + glutamine + NADH → 2 glutamate + NAD^+

and being that encoded by GLT1 of the strain of *Saccharomyces cerevisiae* deposited under DSM Accession No. 12275; and

(c) a glutamine synthetase activity catalyzing the reaction:

glutamate + NH_4^+ + ATP → glutamine + ADP + Pi

and being that encoded by GLN1 of the strain of

Saccharomyces cerevisiae deposited under DSM Accession No. 12274;

wherein each increased enzyme activity is that of

(1) an enzyme, endogenous to said cell, encoded by a nucleic acid coding sequence operably linked to at least one regulatory sequence not natively associated with said nucleic acid coding sequence, whose expression is increased as compared to the expression of the enzyme activity when said nucleic acid coding sequence is associated with its native regulatory sequence, or

(2) an enzyme, exogenous to said cell, encoded by a nucleic acid coding sequence, operably linked to at least one regulatory sequence,

and

wherein the recombinant yeast cell is further characterized by

(ii) a reduced expressible enzyme activity controlling anabolic metabolism of ammonia in said cell as a nutrient source, said reduced enzyme activity being a natively present NADPH-dependent glutamate dehydrogenase activity which reduced activity is reduced compared to the native level of activity.